

Title: US-09-988-202-5

RESULT 1

ACCGKAB

LOCUS ACCGKAB 2180 bp DNA linear BCT 21-APR-1994

DEFINITION A.carrageenovora genes cgkA and cgkB, partial.

ACCESSION X71620

VERSION X71620.1 GI:437973

KEYWORDS kappa-carrageenase.

SOURCE Pseudoalteromonas carrageenovora

ORGANISM Pseudoalteromonas carrageenovora

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

Alteromonadaceae; Pseudoalteromonas.

REFERENCE

1

AUTHORS Barbeyron,T., Henrissat,B. and Kloareg,B.

TITLE The gene encoding the kappa-carrageenase of Alteromonas

carrageenovora is related to beta-1,3-1,4-glucanases

JOURNAL Gene 139 (1), 105-109 (1994)

MEDLINE 94156170

PUBMED 8112578

REFERENCE 2 (bases 1 to 2180)

AUTHORS Barbeyron,T.

TITLE Direct Submission

JOURNAL Submitted (15-APR-1993) T. Barbeyron, CNRS, Place George Teissier,
29680 Roscoff, FRANCE

FEATURES

Location/Qualifiers

source

1..2180

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/db_xref="taxon:227"

/clone="pKA1,pKA2,pKA3,pKA4"

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-35_signal

557..562

/gene="cgkA"

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RBS

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CDS

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gene

2000..2180

/gene="cgkB"

RBS

2000..2004

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CDS

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BASE COUNT 787 a 397 c 420 g 576 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GATCATATCATTCCTTTGCAAATTAAAAATTCTCAAGATAGTCAAATAATTAGTTTTTTT	60
Qy	61	AAAGCTGACAAAGGGAGTGTGAGCAGGCAAGTACACCCACCTTGGCCTGTGCCTTGTA	120
Db	61	AAAGCTGACAAAGGGAGTGTGAGCAGGCAAGTACACCCACCTTGGCCTGTGCCTTGTA	120
Qy	121	AGTAAACTGCAAGAGCAAGATAGTAGTGAGTCTAAAGAGAGTAAGGCAGAGCAAGTTAA	180
Db	121	AGTAAACTGCAAGAGCAAGATAGTAGTGAGTCTAAAGAGAGTAAGGCAGAGCAAGTTAA	180
Qy	181	ATTAACAACTGCGTTGTACAGAACGCAATGCTGTACATAGAAAACAATTATTTCAACGAT	240
Db	181	ATTAACAACTGCGTTGTACAGAACGCAATGCTGTACATAGAAAACAATTATTTCAACGAT	240
Qy	241	ATAAATATAGACACGGTTGCTTTTTCTGTTGGCGTAAGTCGCTCTTATCTCGTTAAACA	300
Db	241	ATAAATATAGACACGGTTGCTTTTTCTGTTGGCGTAAGTCGCTCTTATCTCGTTAAACA	300
Qy	301	TTTAAGTTAGCAACGAATAAAACGATTAATAATAGAATCATAGAAGTAAGAATAGAGCAG	360
Db	301	TTTAAGTTAGCAACGAATAAAACGATTAATAATAGAATCATAGAAGTAAGAATAGAGCAG	360
Qy	361	GCTAAAAAAGTATTACTAAAAAATCTGTTACAGAAACAGCTTATGAAGTTGGTTTTAAT	420
Db	361	GCTAAAAAAGTATTACTAAAAAATCTGTTACAGAAACAGCTTATGAAGTTGGTTTTAAT	420
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Db	421	AACTCAAACACTTTCGCGACAGTTTTTAAAAAAGAACAACACTACACGCCCAAGCAATTT	480
Qy	481	AAACGTACTTTTTCCAGCTAAACTACAATAACGATTAAAGCCATTTTATAGAGA	540
Db	481	AAACGTACTTTTTCCAGCTAAACTACAATAACGATTAAAGCCATTTTATAGAGA	540
Qy	541	ACAGTAAACCATTTTTTGAGGTTTGGTGTGTATATAAATATTAAATATCCCCACTCGC	600
Db	541	ACAGTAAACCATTTTTTGAGGTTTGGTGTGTATATAAATATTAAATATCCCCACTCGC	600
Qy	601	TCAGCTTTTTTTGTGCGAGTTGTGAGAATTAGCTTAACAGGTAAGGTTTACGTATCTGTA	660
Db	601	TCAGCTTTTTTTGTGCGAGTTGTGAGAATTAGCTTAACAGGTAAGGTTTACGTATCTGTA	660
Qy	661	TATCTAAACTCTTCGAATATAACACTGTATCTGTTGCTGAGCTGTGGCTCAGTTCACACT	720
Db	661	TATCTAAACTCTTCGAATATAACACTGTATCTGTTGCTGAGCTGTGGCTCAGTTCACACT	720
Qy	721	AACAAAGGATGGATAAATAAATGAAACCTATAAGTATTGTGGCATTCCCTATACCAGCTA	780
Db	721	AACAAAGGATGGATAAATAAATGAAACCTATAAGTATTGTGGCATTCCCTATACCAGCTA	780
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Db	781	TAAGTATGCTTCTTTTAAGTGCAGTATCACAAGCAGCATCTATGCAACCTCCCATCGCAA	840
Qy	841	AACCTGGTGAAACATGGATTTTACAAGCCAAACGCTCTGACGAATTTAACGTAAAAGATG	900
Db	841	AACCTGGTGAAACATGGATTTTACAAGCCAAACGCTCTGACGAATTTAACGTAAAAGATG	900
Qy	901	CGACAAAGTGGAACCTTCAAACAGAAAACCTATGGGGTATGGTCTTGGA AAAATGAAAATG	960
Db	901	CGACAAAGTGGAACCTTCAAACAGAAAACCTATGGGGTATGGTCTTGGA AAAATGAAAATG	960

Qy	961	CGACAGTATCTAATGGCAAACATAAAATTAACCACTAAGCGAGAATCTCATCAACGTACAT	1020
Db	961	CGACAGTATCTAATGGCAAACATAAAATTAACCACTAAGCGAGAATCTCATCAACGTACAT	1020
Qy	1021	TCTGGGATGGCTGTAATCAGCAGCAAGTTGCAAATTACCCACTTTATTATACATCGGGTG	1080
Db	1021	TCTGGGATGGCTGTAATCAGCAGCAAGTTGCAAATTACCCACTTTATTATACATCGGGTG	1080
Qy	1081	TCGCTAAATCCAGAGCTACAGGTAATTATGGCTATTACGAAGCTCGAATCAAAGGAGCGA	1140
Db	1081	TCGCTAAATCCAGAGCTACAGGTAATTATGGCTATTACGAAGCTCGAATCAAAGGAGCGA	1140
Qy	1141	GTACATTTCTGGCGTATCGCCTGCTTTTTGGATGTATAGCACCATTGACCGTTCATTAA	1200
Db	1141	GTACATTTCTGGCGTATCGCCTGCTTTTTGGATGTATAGCACCATTGACCGTTCATTAA	1200
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Db	1201	CGAAAGAAGGGGATGTCCAATATAGCGAAATAGACGTAGTGGAACCTTACTCAAAAAAGTG	1260
Qy	1261	CAGTGAGAGAGTCTGATCATGACTTACACAATATTGTAGTAAAAAATGGAAAACCAACAT	1320
Db	1261	CAGTGAGAGAGTCTGATCATGACTTACACAATATTGTAGTAAAAAATGGAAAACCAACAT	1320
Qy	1321	GGATGCGTCCAGGGTCTTTTCCGCAGACAAATCATAACGGATACCATCTACCTTTCGATC	1380
Db	1321	GGATGCGTCCAGGGTCTTTTCCGCAGACAAATCATAACGGATACCATCTACCTTTCGATC	1380
Qy	1381	CTCGAAATGACTTTCACACCTATGGTGTCAATGTAACATAAGACAAGATCACTTGGTACG	1440
Db	1381	CTCGAAATGACTTTCACACCTATGGTGTCAATGTAACATAAGACAAGATCACTTGGTACG	1440
Qy	1441	TAGATGGTGAAATTGTGGGCGAAAAGGATAACTTATACTGGCATCGTCAAATGAATCTCA	1500
Db	1441	TAGATGGTGAAATTGTGGGCGAAAAGGATAACTTATACTGGCATCGTCAAATGAATCTCA	1500
Qy	1501	CATTATCACAAGGCTTACGCGCGCCGCATACACAATGGAAATGTAATCAATTTTACCCAT	1560
Db	1501	CATTATCACAAGGCTTACGCGCGCCGCATACACAATGGAAATGTAATCAATTTTACCCAT	1560
Qy	1561	CAGCGAATAAATCAGCAGAAGGCTTCCCAACATCAATGGAAGTTGATTATGTAAGAACGT	1620
Db	1561	CAGCGAATAAATCAGCAGAAGGCTTCCCAACATCAATGGAAGTTGATTATGTAAGAACGT	1620
Qy	1621	GGGTAAAGGTGGGCAATAACAACCTCTGCTCCAGGCGAGGGGCAGTCATGTCCTAACACGT	1680
Db	1621	GGGTAAAGGTGGGCAATAACAACCTCTGCTCCAGGCGAGGGGCAGTCATGTCCTAACACGT	1680
Qy	1681	TTGTAGCTGTCAATAGTGTTCAACTAAGCGCAGCAAAACAAACACTTCGAAAGGGCCAAT	1740
Db	1681	TTGTAGCTGTCAATAGTGTTCAACTAAGCGCAGCAAAACAAACACTTCGAAAGGGCCAAT	1740
Qy	1741	CTACAACGCTAGAAAGCACAGTTCTTCCAAACTGTGCAACCAACAAGAAAGTCATTTATT	1800
Db	1741	CTACAACGCTAGAAAGCACAGTTCTTCCAAACTGTGCAACCAACAAGAAAGTCATTTATT	1800
Qy	1801	CATCAAGCAATAAAAATGTGGCAACTGTGAACAGTGCTGGCGTTGTAAAAGCTAAAAATA	1860
Db	1801	CATCAAGCAATAAAAATGTGGCAACTGTGAACAGTGCTGGCGTTGTAAAAGCTAAAAATA	1860
Qy	1861	AAGGCACTGCGACGATTACGGTTAAACTAAAAACAAAGGGAAAATAGATAAATTAACCA	1920
Db	1861	AAGGCACTGCGACGATTACGGTTAAACTAAAAACAAAGGGAAAATAGATAAATTAACCA	1920
Qy	1921	TTGCGGTGAATTAAGCTAACTCAAAGCTAGCCTCGAAGGATTGAGGCACTTTATTTATAGG	1980
Db	1921	TTGCGGTGAATTAAGCTAACTCAAAGCTAGCCTCGAAGGATTGAGGCACTTTATTTATAGG	1980
Qy	1981	TCTCAGGCTTCGACTTTTTGGAGGGGGTATGAAAAAGGTAAATTTATCCAGCAAGTGGAT	2040
Db	1981	TCTCAGGCTTCGACTTTTTGGAGGGGGTATGAAAAAGGTAAATTTATCCAGCAAGTGGAT	2040

Qy	2041	AATTAGCATTAGTTTACTAATCATTGTGATTATGTTTATTTAATACGAACAAACGTTAA	2100
Db	2041	AATTAGCATTAGTTTACTAATCATTGTGATTATGTTTATTTAATACGAACAAACGTTAA	2100
Qy	2101	CGAGCAAGCTAACGCAGAAGCTACTGCACATATGCATTACAAAATAAATAATACGAAACA	2160
Db	2101	CGAGCAAGCTAACGCAGAAGCTACTGCACATATGCATTACAAAATAAATAATACGAAACA	2160
Qy	2161	CTCAAAAGGAAAGCTTGATC	2180
Db	2161	CTCAAAAGGAAAGCTTGATC	2180

Title: US-09-988-202-6

RESULT 1

I39507

kappa-carraghenase - *Alteromonas carrageenovora*

C;Species: *Alteromonas carrageenovora*

C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 08-Oct-1999

C;Accession: I39507; S40202

R;Barbeyron, T.; Henrissat, B.; Kloareg, B.

Gene 139, 105-109, 1994

A;Title: The gene encoding the kappa-carrageenase of *Alteromonas carrageenovora* is related to beta-1,3-1,4-glucanases.

A;Reference number: I39507; MUID:94156170; PMID:8112578

A;Accession: I39507

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-397 <RES>

A;Cross-references: EMBL:X71620; NID:g437973; PIDN:CAA50624.1; PID:g437974

C;Genetics:

A;Gene: cgkA

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Matches 397; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	227	TENYGVWSWKNNENATVSNGKLKLTTKRESHQRTFWDGCNQQQVANYPLYTSGVAKSRAT	286
Db	61	TENYGVWSWKNNENATVSNGKLKLTTKRESHQRTFWDGCNQQQVANYPLYTSGVAKSRAT	120
Qy	287	GNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRES DH	346
Db	121	GNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRES DH	180
Qy	347	DLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVG	406
Db	181	DLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVG	240
Qy	407	EKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKVGNN	466
Db	241	EKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKVGNN	300
Qy	467	NSAPGEGQSCPNTFVAVNSVQLSAAKQTLRKGQSTTLESTVLPNCATNKKVIYSSSNKNV	526
Db	301	NSAPGEGQSCPNTFVAVNSVQLSAAKQTLRKGQSTTLESTVLPNCATNKKVIYSSSNKNV	360
Qy	527	ATVNSAGVVKAKNKG TATITVKTKNKGKIDKLTIAVN	563
Db	361	ATVNSAGVVKAKNKG TATITVKTKNKGKIDKLTIAVN	397